

PATENT APPLICATION File No.: 98-10D1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Wen-feng Xu, Scott R. Presnell, David P.

Yee, Donald C. Foster

Serial No.: 09/371,333 Group Art Unit: 1646

Filed: August 10, 1999 Examiner: John D. Ulm

For: PROTEASE-ACTIVATED RECEPTOR PAR4 (ZCHEMR2)

LETTER REGARDING SUBSTITUTE SEQUENCE LISTING

Commissioner for Patents Washington, DC 20231

Sir:

Submitted herewith is a substitute copy of the sequence listing. The substitute sequence listing contains no new matter and is now compliant with the revised sequence rules under 37 C.F.R. § 1.821-1.825.

Also submitted herewith is a sequence listing diskette for the above-captioned application. The content of substitute sequence listing and the enclosed sequence listing diskette is the same and, where applicable, includes no new matter as required by 37 CFR 1.821-1.825.

Respectfully submitted,

Phillip B.C. Jones, J.D., Ph.D.

Registration No. 38,195



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SEQUENCE LISTING

<110> Xu, Wenfeng
 Presnell, Scott R.
 Yee, David P.
 Foster, Donald C.

<120> PROTEASE-ACTIVATED RECEPTOR PAR4 (ZCHEMR2)

<130> 98-10D1

<140> US 09/371,333

<141> 1999-08-10

<150> US 09/053,866

<151> 1998-04-01

<160> 21

<170> FastSEQ for Windows Version 3.0

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<211> 4895

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)...(1330)

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ggtccggcga ggcaggaagc ctgaggccac agcccagagc agcctgagtg cagtc atg 178

Met

1

05

tgg ggg cga ctg ctc ctg tgg ccc ctg gtg ctg ggg ttc agc ctg tct 226

Trp Gly Arg Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser 5 10 15

ggc ggc acc cag acc ccc agc gtc tac gac gag agc ggg agc acc gga 274

Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly 20 25 30

ggt ggt gat gac agc acg ccc tca atc ctg cct gcc ccc cgc ggc tac 322

Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr 35 40 45

cca ggc caa gtc tgt gcc aat gac agt gac acc ctg gag ctc ccg gac 370

Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp 50 55 60 65

age tea egg gea etg ett etg gge tgg gtg eec ace agg etg gtg eec 418

Ser Ser Arg Ala Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro 70 75 80

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Ala Leu Tyr Gly Leu Val Leu Val Gly Leu Pro Ala Asn Gly Leu 85 90 95

gcg ctg tgg gtg ctg gcc acg cag gca cct cgg ctg ccc tcc acc atg 514

Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
100 105 110

ctg ctg atg aac ctc gcg act gct gac ctc ctg ctg gcc ctg gcg ctg 562

Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu 115 120 125

ccc ccg cgg atc gcc tac cac ctg cgt ggc cag cgc tgg ccc ttc ggg 610

Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe Gly qaq gcc gcc tgc cgc ctg gcc acg gcc gca ctc tat ggt cac atg tat Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met Tyr ggc tca gtg ctg ctg gcc gcc gtc agc ctg gat cgc tac ctg gcc Gly Ser Val Leu Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala ctg gtg cac ccg ctg cgg gcc cgc gcc ctg cgt ggc cgg cgc ctg gcc Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu Ala ctt gga ctc tgc atg gct gct tgg ctc atg gcg gcc gcc ctg gca ctg Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala Leu ccc ctg aca ctg cag cgg cag acc ttc cgg ctg gcg cgc tcc gat cgc Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp Arg gtg ctc tgc cat gac gcg ctg ccc ctg gac gca cag gcc tcc cac tgg Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His Trp caa ccg gcc ttc acc tgc ctg gcg ctg ttg ggc tgt ttc ctg ccc ctg Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro Leu ctq gcc atg ctg tgc tac ggg gcc acc ctg cac acg ctg gcg gcc Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala Ala

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gcc tcc gcc gtg gcc ttc ttc gtg ccc agc aac ctg ctg ctg ctg 1090

Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu 290 295 300 305

cat tac tcg gac ccg agc ccc agc gcc tgg ggc aac ctc tat ggt gcc 1138

His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly Ala 310 315 320

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Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp Pro 325 330 335

ttc atc tac tac gtg tcg gcc gag ttc agg gac aag gtg cgg gca 1234

Phe Ile Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg Ala 340 345 350

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Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu Gln 370 380 385

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4690
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                                                      15
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            20
                               25
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Gly	Gly	G1y 35	Asp	Asp	Ser	Thr	Pro 40	Ser	Пе	Leu	Pro	A1a 45	Pro	Arg	Gly
Tyr	Pro 50	Gly	Gln	Val	Cys	Ala 55	Asn	Asp	Ser	Asp	Thr 60	Leu	Glu	Leu	Pro
Asp 65	Ser	Ser	Arg	Ala	Leu 70	Leu	Leu	Gly	Trp	Va1 75	Pro	Thr	Arg	Leu	Val 80
Pro	Ala	Leu	Tyr	Gly 85	Leu	Val	Leu	Val	Va1 90	Gly	Leu	Pro	Ala	Asn 95	Gly
Leu	Ala	Leu	Trp 100	Val	Leu	Ala	Thr	Gln 105	Ala	Pro	Arg	Leu	Pro 110	Ser	Thr
		Leu 115					120					125			
	130	Pro				135					140		·		
145		Ala		-	150					155		_	_		160
	_	Ser		165					170			·		175	
		Val	180					185					190		
		Gly 195					200					205			
	210	Leu				215					220				·
225		Leu	-		230					235					240
		Pro		245					250		-	_		255	
		Ala	260					265					270		
		G1y 275					280					285			
	290	Ser				295					300				
305		Tyr		·	310					315					320
		Val		325					330					335	
		Ile	340					345				·	350		-
АІа	ыу	Leu 355	rne	GIN	Arg	5er	360	ыу	Asp	ınr	val	365	Ser	Lys	Ala

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                         375
                                             380
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 G1n
 385
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       <212> DNA
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       <222> (1)...(1155)
       <223> N is any nucleotide.
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 gtnytngcna cncargenec nmgnytnech wsnachatgy tnytnatgaa yytngcnach
360
 gengayytny tnytngenyt ngenytneen cenmgnathg entayeayyt nmgnggnear
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 tayggnwsng tnytnytnyt ngcngcngtn wsnytngaym gntayytngc nytngtncay
540
 conythmana chmanachyt hmanaghman manythachy thaganythta yatagchach
 tggytnatgg engengenyt ngenytneen ytnaenytne armgnearae nttymgnytn
660
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genmgnwsng aymgngtnyt ntgycaygay genytneeny tngaygenea rgenwsneay
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780
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 genythmgny thachgengt ngthythgen wsngengthg enttyttygt nechwshaay
900
ytnytnytny tnytncayta ywsngayccn wsnccnwsng cntggggnaa yytntayggn
960
gcntaygtnc cnwsnytngc nytnwsnacn ytnaaywsnt gygtngaycc nttyathtay
1020
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1080
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 1
                  5
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                                                         15
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Ser Phe Leu Leu Arg Asn
                 5
 1
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22
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9
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                                     10
Asp Thr Leu Glu Leu Pro Asp Ser Ser
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CS Cont